RAW SEQUENCE LISTING   DATE: 09/26/2001
PATENT APPLICATION: **US/09/942,021**   TIME: 13:55:27

Input Set : **N:\Crf3\RULE60\09942021.txt**
Output Set: **N:\CRF3\09262001\I942021.raw**

SEQUENCE LISTING
4 (1) GENERAL INFORMATION:
6   (i) APPLICANT: Little, Roger G. II
8   (ii) TITLE OF INVENTION: Therapeutic Uses of Bactericidal/Permeability
9   Increasing (BPI) Protein Products
11   (iii) NUMBER OF SEQUENCES: 2
13   (iv) CORRESPONDENCE ADDRESS:
14   (A) ADDRESSEE: McAndrews, Held & Malloy, Ltd.
15   (B) STREET: 500 W. Madison Street, 34th Floor
16   (C) CITY: Chicago
17   (D) STATE: Illinois
18   (E) COUNTRY: USA
19   (F) ZIP: 60661
21   (v) COMPUTER READABLE FORM:
22   (A) MEDIUM TYPE: Floppy disk
23   (B) COMPUTER: IBM PC compatible
24   (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25   (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
27   (vi) CURRENT APPLICATION DATA:
C--> 28   **(A) APPLICATION NUMBER: US/09/942,021**
C--> 29   **(B) FILING DATE: 27-Aug-2001**
30   (C) CLASSIFICATION:
44   (vii) PRIOR APPLICATION DATA:
33   (A) APPLICATION NUMBER: 09/220,427
34   (B) FILING DATE: 24-DEC-1998
37   (A) APPLICATION NUMBER: 08/415,158
38   (B) FILING DATE: March 31, 1995
41   (A) APPLICATION NUMBER: 08/093,202
42   (B) FILING DATE: July 15, 1993
45   (A) APPLICATION NUMBER: 08/030,644
46   (B) FILING DATE: March 12, 1993
C--> 48   **(viii) ATTORNEY/AGENT INFORMATION:**
49   (A) NAME: McNicholas, Janet M.
50   (B) REGISTRATION NUMBER: 32,918
51   (C) REFERENCE/DOCKET NUMBER: 11004US07 / 100-224.P1.C3
53   (ix) TELECOMMUNICATION INFORMATION:
54   (A) TELEPHONE: 312/707-8889
55   (B) TELEFAX: 312/707-9155
56   (C) TELEX:
59 (2) INFORMATION FOR SEQ ID NO: 1:
61   (i) SEQUENCE CHARACTERISTICS:
62   (A) LENGTH: 1813 base pairs
63   (B) TYPE: nucleic acid
64   (C) STRANDEDNESS: single
65   (D) TOPOLOGY: linear
67   (ii) MOLECULE TYPE: cDNA
69   (ix) FEATURE:

ENTERED

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70              (A) NAME/KEY: CDS
71              (B) LOCATION: 31..1491
73          (ix) FEATURE:
74              (A) NAME/KEY: mat_peptide
75              (B) LOCATION: 124..1491
77          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
79 CAGGCCTTGA GGTTTTGGCA GCTCTGGAGG ATG AGA GAG AAC ATG GCC AGG GGC          54
80                                   Met Arg Glu Asn Met Ala Arg Gly
81                                   -31 -30                    -25
83 CCT TGC AAC GCG CCG AGA TGG GTG TCC CTG ATG GTG CTC GTC GCC ATA          102
84 Pro Cys Asn Ala Pro Arg Trp Val Ser Leu Met Val Leu Val Ala Ile
85           -20                 -15                 -10
87 GGC ACC GCC GTG ACA GCG GCC GTC AAC CCT GGC GTC GTG GTC AGG ATC          150
88 Gly Thr Ala Val Thr Ala Ala Val Asn Pro Gly Val Val Val Arg Ile
89           -5                  1                   5
91 TCC CAG AAG GGC CTG GAC TAC GCC AGC CAG CAG GGG ACG GCC GCT CTG          198
92 Ser Gln Lys Gly Leu Asp Tyr Ala Ser Gln Gln Gly Thr Ala Ala Leu
93   10                  15                  20                  25
95 CAG AAG GAG CTG AAG AGG ATC AAG ATT CCT GAC TAC TCA GAC AGC TTT          246
96 Gln Lys Glu Leu Lys Arg Ile Lys Ile Pro Asp Tyr Ser Asp Ser Phe
97                   30                  35                  40
99 AAG ATC AAG CAT CTT GGG AAG GGG CAT TAT AGC TTC TAC AGC ATG GAC          294
100 Lys Ile Lys His Leu Gly Lys Gly His Tyr Ser Phe Tyr Ser Met Asp
101              45                  50                  55
103 ATC CGT GAA TTC CAG CTT CCC AGT TCC CAG ATA AGC ATG GTG CCC AAT          342
104 Ile Arg Glu Phe Gln Leu Pro Ser Ser Gln Ile Ser Met Val Pro Asn
105             60                  65                  70
107 GTG GGC CTT AAG TTC TCC ATC AGC AAC GCC AAT ATC AAG ATC AGC GGG          390
108 Val Gly Leu Lys Phe Ser Ile Ser Asn Ala Asn Ile Lys Ile Ser Gly
109     75                  80                  85
111 AAA TGG AAG GCA CAA AAG AGA TTC TTA AAA ATG AGC GGC AAT TTT GAC          438
112 Lys Trp Lys Ala Gln Lys Arg Phe Leu Lys Met Ser Gly Asn Phe Asp
113 90                  95                  100                 105
115 CTG AGC ATA GAA GGC ATG TCC ATT TCG GCT GAT CTG AAG CTG GGC AGT          486
116 Leu Ser Ile Glu Gly Met Ser Ile Ser Ala Asp Leu Lys Leu Gly Ser
117                 110                 115                 120
119 AAC CCC ACG TCA GGC AAG CCC ACC ATC ACC TGC TCC AGC TGC AGC AGC          534
120 Asn Pro Thr Ser Gly Lys Pro Thr Ile Thr Cys Ser Ser Cys Ser Ser
121                 125                 130                 135
123 CAC ATC AAC AGT GTC CAC GTG CAC ATC TCA AAG AGC AAA GTC GGG TGG          582
124 His Ile Asn Ser Val His Val His Ile Ser Lys Ser Lys Val Gly Trp
125             140                 145                 150
127 CTG ATC CAA CTC TTC CAC AAA AAA ATT GAG TCT GCG CTT CGA AAC AAG          630
128 Leu Ile Gln Leu Phe His Lys Lys Ile Glu Ser Ala Leu Arg Asn Lys
129     155                 160                 165
131 ATG AAC AGC CAG GTC TGC GAG AAA GTG ACC AAT TCT GTA TCC TCC AAG          678
132 Met Asn Ser Gln Val Cys Glu Lys Val Thr Asn Ser Val Ser Ser Lys
133 170                 175                 180                 185
135 CTG CAA CCT TAT TTC CAG ACT CTG CCA GTA ATG ACC AAA ATA GAT TCT          726
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```
136 Leu Gln Pro Tyr Phe Gln Thr Leu Pro Val Met Thr Lys Ile Asp Ser
137                 190                 195                 200
139 GTG GCT GGA ATC AAC TAT GGT CTG GTG GCA CCT CCA GCA ACC ACG GCT      774
140 Val Ala Gly Ile Asn Tyr Gly Leu Val Ala Pro Pro Ala Thr Thr Ala
141                 205                 210                 215
143 GAG ACC CTG GAT GTA CAG ATG AAG GGG GAG TTT TAC AGT GAG AAC CAC      822
144 Glu Thr Leu Asp Val Gln Met Lys Gly Glu Phe Tyr Ser Glu Asn His
145             220                 225                 230
147 CAC AAT CCA CCT CCC TTT GCT CCA CCA GTG ATG GAG TTT CCC GCT GCC      870
148 His Asn Pro Pro Pro Phe Ala Pro Pro Val Met Glu Phe Pro Ala Ala
149             235                 240                 245
151 CAT GAC CGC ATG GTA TAC CTG GGC CTC TCA GAC TAC TTC TTC AAC ACA      918
152 His Asp Arg Met Val Tyr Leu Gly Leu Ser Asp Tyr Phe Phe Asn Thr
153 250                 255                 260                 265
155 GCC GGG CTT GTA TAC CAA GAG GCT GGG GTC TTG AAG ATG ACC CTT AGA      966
156 Ala Gly Leu Val Tyr Gln Glu Ala Gly Val Leu Lys Met Thr Leu Arg
157                 270                 275                 280
159 GAT GAC ATG ATT CCA AAG GAG TCC AAA TTT CGA CTG ACA ACC AAG TTC     1014
160 Asp Asp Met Ile Pro Lys Glu Ser Lys Phe Arg Leu Thr Thr Lys Phe
161             285                 290                 295
163 TTT GGA ACC TTC CTA CCT GAG GTG GCC AAG AAG TTT CCC AAC ATG AAG     1062
164 Phe Gly Thr Phe Leu Pro Glu Val Ala Lys Lys Phe Pro Asn Met Lys
165             300                 305                 310
167 ATA CAG ATC CAT GTC TCA GCC TCC ACC CCG CCA CAC CTG TCT GTG CAG     1110
168 Ile Gln Ile His Val Ser Ala Ser Thr Pro Pro His Leu Ser Val Gln
169     315                 320                 325
171 CCC ACC GGC CTT ACC TTC TAC CCT GCC GTG GAT GTC CAG GCC TTT GCC     1158
172 Pro Thr Gly Leu Thr Phe Tyr Pro Ala Val Asp Val Gln Ala Phe Ala
173 330                 335                 340                 345
175 GTC CTC CCC AAC TCC TCC CTG GCT TCC CTC TTC CTG ATT GGC ATG CAC     1206
176 Val Leu Pro Asn Ser Ser Leu Ala Ser Leu Phe Leu Ile Gly Met His
177                 350                 355                 360
179 ACA ACT GGT TCC ATG GAG GTC AGC GCC GAG TCC AAC AGG CTT GTT GGA     1254
180 Thr Thr Gly Ser Met Glu Val Ser Ala Glu Ser Asn Arg Leu Val Gly
181             365                 370                 375
183 GAG CTC AAG CTG GAT AGG CTG CTC CTG GAA CTG AAG CAC TCA AAT ATT     1302
184 Glu Leu Lys Leu Asp Arg Leu Leu Leu Glu Leu Lys His Ser Asn Ile
185             380                 385                 390
187 GGC CCC TTC CCG GTT GAA TTG CTG CAG GAT ATC ATG AAC TAC ATT GTA     1350
188 Gly Pro Phe Pro Val Glu Leu Leu Gln Asp Ile Met Asn Tyr Ile Val
189     395                 400                 405
191 CCC ATT CTT GTG CTG CCC AGG GTT AAC GAG AAA CTA CAG AAA GGC TTC     1398
192 Pro Ile Leu Val Leu Pro Arg Val Asn Glu Lys Leu Gln Lys Gly Phe
193 410                 415                 420                 425
195 CCT CTC CCG ACG CCG GCC AGA GTC CAG CTC TAC AAC GTA GTG CTT CAG     1446
196 Pro Leu Pro Thr Pro Ala Arg Val Gln Leu Tyr Asn Val Val Leu Gln
197             430                 435                 440
199 CCT CAC CAG AAC TTC CTG CTG TTC GGT GCA GAC GTT GTC TAT AAA         1491
200 Pro His Gln Asn Phe Leu Leu Phe Gly Ala Asp Val Val Tyr Lys
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```
201            445              450              455
203 TGAAGGCACC AGGGGTGCCG GGGGCTGTCA GCCGCACCTG TTCCTGATGG GCTGTGGGGC   1551
205 ACCGGCTGCC TTTCCCCAGG GAATCCTCTC CAGATCTTAA CCAAGAGCCC CTTGCAAACT   1611
207 TCTTCGACTC AGATTCAGAA ATGATCTAAA CACGAGGAAA CATTATTCAT TGGAAAAGTG   1671
209 CATGGTGTGT ATTTTAGGGA TTATGAGCTT CTTTCAAGGG CTAAGGCTGC AGAGATATTT   1731
211 CCTCCAGGAA TCGTGTTTCA ATTGTAACCA AGAAATTTCC ATTTGTGCTT CATGAAAAAA   1791
213 AACTTCTGGT TTTTTTCATG TG                                            1813
216 (2) INFORMATION FOR SEQ ID NO: 2:
218      (i) SEQUENCE CHARACTERISTICS:
219          (A) LENGTH: 487 amino acids
220          (B) TYPE: amino acid
221          (D) TOPOLOGY: linear
223     (ii) MOLECULE TYPE: protein
225     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
227 Met Arg Glu Asn Met Ala Arg Gly Pro Cys Asn Ala Pro Arg Trp Val
228 -31 -30              -25                -20
230 Ser Leu Met Val Leu Val Ala Ile Gly Thr Ala Val Thr Ala Ala Val
231 -15             -10              -5                          1
233 Asn Pro Gly Val Val Val Arg Ile Ser Gln Lys Gly Leu Asp Tyr Ala
234             5              10                15
236 Ser Gln Gln Gly Thr Ala Ala Leu Gln Lys Glu Leu Lys Arg Ile Lys
237         20              25              30
239 Ile Pro Asp Tyr Ser Asp Ser Phe Lys Ile Lys His Leu Gly Lys Gly
240     35              40                  45
242 His Tyr Ser Phe Tyr Ser Met Asp Ile Arg Glu Phe Gln Leu Pro Ser
243 50              55                60                          65
245 Ser Gln Ile Ser Met Val Pro Asn Val Gly Leu Lys Phe Ser Ile Ser
246             70              75                  80
248 Asn Ala Asn Ile Lys Ile Ser Gly Lys Trp Lys Ala Gln Lys Arg Phe
249             85              90                  95
251 Leu Lys Met Ser Gly Asn Phe Asp Leu Ser Ile Glu Gly Met Ser Ile
252         100             105             110
254 Ser Ala Asp Leu Lys Leu Gly Ser Asn Pro Thr Ser Gly Lys Pro Thr
255     115             120             125
257 Ile Thr Cys Ser Ser Cys Ser Ser His Ile Asn Ser Val His Val His
258 130             135             140                         145
260 Ile Ser Lys Ser Lys Val Gly Trp Leu Ile Gln Leu Phe His Lys Lys
261             150             155             160
263 Ile Glu Ser Ala Leu Arg Asn Lys Met Asn Ser Gln Val Cys Glu Lys
264             165             170             175
266 Val Thr Asn Ser Val Ser Ser Lys Leu Gln Pro Tyr Phe Gln Thr Leu
267         180             185             190
269 Pro Val Met Thr Lys Ile Asp Ser Val Ala Gly Ile Asn Tyr Gly Leu
270     195             200             205
272 Val Ala Pro Pro Ala Thr Thr Ala Glu Thr Leu Asp Val Gln Met Lys
273 210             215             220             225
275 Gly Glu Phe Tyr Ser Glu Asn His His Asn Pro Pro Pro Phe Ala Pro
276             230             235             240
278 Pro Val Met Glu Phe Pro Ala Ala His Asp Arg Met Val Tyr Leu Gly
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```
279           245                 250                 255
281 Leu Ser Asp Tyr Phe Phe Asn Thr Ala Gly Leu Val Tyr Gln Glu Ala
282         260                 265                 270
284 Gly Val Leu Lys Met Thr Leu Arg Asp Asp Met Ile Pro Lys Glu Ser
285         275                 280                 285
287 Lys Phe Arg Leu Thr Thr Lys Phe Phe Gly Thr Phe Leu Pro Glu Val
288 290                 295                 300                 305
290 Ala Lys Lys Phe Pro Asn Met Lys Ile Gln Ile His Val Ser Ala Ser
291                 310                 315                 320
293 Thr Pro Pro His Leu Ser Val Gln Pro Thr Gly Leu Thr Phe Tyr Pro
294         325                 330                 335
296 Ala Val Asp Val Gln Ala Phe Ala Val Leu Pro Asn Ser Ser Leu Ala
297         340                 345                 350
299 Ser Leu Phe Leu Ile Gly Met His Thr Thr Gly Ser Met Glu Val Ser
300         355                 360                 365
302 Ala Glu Ser Asn Arg Leu Val Gly Glu Leu Lys Leu Asp Arg Leu Leu
303 370                 375                 380                 385
305 Leu Glu Leu Lys His Ser Asn Ile Gly Pro Phe Pro Val Glu Leu Leu
306                 390                 395                 400
308 Gln Asp Ile Met Asn Tyr Ile Val Pro Ile Leu Val Leu Pro Arg Val
309                 405                 410                 415
311 Asn Glu Lys Leu Gln Lys Gly Phe Pro Leu Pro Thr Pro Ala Arg Val
312         420                 425                 430
314 Gln Leu Tyr Asn Val Val Leu Gln Pro His Gln Asn Phe Leu Leu Phe
315         435                 440                 445
317 Gly Ala Asp Val Val Tyr Lys
318 450                 455
```

VERIFICATION SUMMARY   DATE: 09/26/2001
PATENT APPLICATION: **US/09/942,021**   TIME: 13:55:28

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Output Set: **N:\CRF3\09262001\I942021.raw**

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:48 M:220 C: Keyword misspelled or invalid format, [(viii) ATTORNEY/AGENT INFORMATION:]